

SEQUENCE LISTING

<110> JOHNS HOPKINS UNIVERSITY

<120> ENHANCEMENT OF ADENOVIRAL ONCOLYTIC ACTIVITY IN
PROSTATE CELLS BY MODIFICATION OF THE E1A GENE PRODUCT

<130> 71699/59562-PCT

<140> PCT/US03/25171

<141> 2003-08-08

<150> 60/401,919

<151> 2002-08-08

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 3768

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial
nucleotide sequence const

<400> 1

accgggactg aaaatgagac atattatctg ccacggaggt gttattaccg aagaaatggc 60
cgccagtctt ttggaccagc tgatcgaaga ggtactggct gataatcttc cacctcctag 120
ccattttgaa ccacctaccc ttcacgaact gtatgattta gacgtgacgg cccccgaaga 180
tcccaacgag gaggcgggtt cgcagatttt tcccgaactct gtaatgttgg cgggtgcagga 240
agggattgac ttactcactt ttccgcgggc gcccggttct ccggagccgc ctccaccttc 300
ccggcagccc gagcagccgg agcagagagc cttgggtccg gtttctatgc caaaccttgc 360
accggaggtg atcgatctta cctgccacga ggctggcttt ccacccagtg acgacgagga 420
tgaagagggg gaggagtttg tgtagatta tgtggagcac ccggggcacg gttgcaggtc 480
ttgtcattat caccggagga atacggggga ccagatatt atgtgttcgc tttgctatat 540
gaggacctgt ggcattgttg tctacagtaa gtgaaaatta tgggcagtgg gtgatagagt 600
ggtgggtttg gtgtggtaat ttttttttta atttttacag ttttgtggtt taaagaattt 660
tgtattgtga tttttttaaa aggtcctgtg tctgaacctg agcctgagcc cgagccagaa 720
ccggagcctg caagacctac ccgcccctct aaaatggcgc ctgctatcct gagacgcccg 780
acatcacctg tgtctagaga atgcaatagt agtacggata gctgtgactc cggtccttct 840

aacacacctc ctgagataca cccggtgggc ccgctgtgcc ccattaaacc agttgccgtg 900
agagttggtg ggcgtcgcca ggctgtggaa tgtatcgagg acttgcttaa cgagcctggg 960
caaccttttg acttgagctg taaacgcccc aggccagcgg ccgcagaagt gcagttaggg 1020
ctgggaaggg tctacctcgc gccgcgctcc aagacctacc gaggagcttt ccagaatctg 1080
ttccagagcg tgcgcgaagt gatccagaac ccgggccccca ggcacccaga ggccgcgagc 1140
gcagcacctc ccggcgccag tttgctgctg ctgcagcagc agcagcagca gcagcagcag 1200
cagcagcagc agcagcagca gcagcagcag cagcaagaga ctagccccag gcagcagcag 1260
cagcagcagg gtgaggatgg ttctcccaa gccatcgta gagggccccc aggtctacctg 1320
gtcctggatg aggaacagca accttcacag ccgcagtcgg ccctggagtg ccaccccgag 1380
agaggttgcg tcccagagcc tggagccgcc gtggccgcca gcaaggggct gccgcagcag 1440
ctgccagcac ctccggacga ggatgactca gctgccccat ccacgttgct cctgctgggc 1500

```

cccactttcc ccggcttaag cagctgctcc gctgacctta aagacatcct gagcgaggcc 1560
agcaccatgc aactccttca gcaacagcag caggaagcag tatccgaagg cagcagcagc 1620
gggagagcga gggaggcctc gggggctccc acttctctca aggacaatta cttagggggc 1680
acttcgacca tttctgacaa cgccaaggag ttgtgtaagg cagtgtcggg gtccatgggc 1740
ctgggtgtgg aggcgttgga gcatctgagt ccaggggaac agcttcgggg ggattgcatg 1800
tacgccccac ttttgggagt tccaccgct gtgctgctcca ctcttctgtc cccattggcc 1860
gaatgcaaag gttctctgct agacgacagc gcaggcaaga gcaactgaaga tactgtgag 1920
tattcccctt tcaagggagg ttacacaaa gggctagaag gcgagagcct aggctgctct 1980
ggcagcgctg cagcaggagg ctccgggaca cttgaactgc cgtctaccct gtctctctac 2040
aagtccggag cactggagca ggcagctgcg taccagagtc gcgactacta caactttcca 2100
ctggctctgg ccggaccgcc gcccctccg ccgcctcccc atccccacgc tcgcatcaag 2160
ctggagaacc cgctggacta cggcagcgcc tggcgggctg cggcggcgca gtgccgctat 2220
ggggacctgg cgagcctgca tggcgcggtg gcagcgggac ccggttcttg gtcaccctca 2280
gccgcccgtt cctcatcctg gcacactctc ttacagccg aagaaggcca gttgtatgga 2340
ccgtgtggtg gtggtggggg tgggtggcggc ggcggcgggc gcggcgggcg cggcgggcg 2400
ggcgggcgcg gcggcggcga ggcgggagct gtgaccccc acggctacac tcggccccct 2460
caggggctgg cgggccaagg aagcgacttc accgcacctg atgtgtggtg ccctggcggc 2520
atggtgagca gagtgcccta tcccagtcct acttgtgtca aaagcgaaat gggccccctg 2580
atggatagct actccggacc ttacggggac atgctgttgg agactgccag ggaccatgtt 2640
ttgcccattg actattactt tccacccag aagacctgcc tgatctgtgg agatgaagct 2700
tctgggtgtc actatggagc tctcacatgt ggaagctgca aggtcttctt caaaagagcc 2760
gctgaaggga aacagaagta cctgtgcgcc agcagaaatg attgcactat tgataaattc 2820
cgaaggaaaa attgtccatc ttgtcgtctt cggaaatgtt atgaagcagg gatgactctg 2880
ggagcccgga agctgaagaa acttggtaat ctgaaactac aggaggaagg agaggcttcc 2940
agcaccacca gcccactga ggagacaacc cagaagctga cagtgtcaca cattgaaggc 3000
tatgaatgtc agcccactct tctgaatgtc ctggaagcca ttgagccagg tgtagtgtgt 3060
gctggacacg acaacaacca gcccgactcc tttgcagcct tgctctctag cctcaatgaa 3120
ctggggagaga gacagcttgt acacgtggtc aagtgggcca aggccttgcc tggcttccgc 3180
aacttacacg tggacgacca gatggctgtc attcagctact cctggatggg gctcatgggtg 3240
tttgccatgg gctggcgatc cttaccaat gtcaactcca ggatgctcta cttcgccccct 3300
gatctgggtt tcaatgagta ccgcatgcac aagtcgccga tgtacagcca gtgtgtccga 3360
atgaggcacc tctctcaaga gtttggatgg ctccaaatca cccccagga attcctgtgc 3420
atgaaagcac tgctactctt cagcattatt ccagtggatg ggctgaaaaa tcaaaaattc 3480
tttgatgaac ttcgaatgaa ctacatcaag gaactcgatc gtatcattgc atgcaaaaaga 3540
aaaaatccca catcctgctc aagacgcttc taccagctca ccaagctcct ggactccgtg 3600
cagcctattg cgagagagct gcatcagttc acttttgacc tgctaataca gtcacacatg 3660
gtgagcgtgg actttccgga aatgatggca gagatcatct ctgtgcaagt gcccaagatc 3720
ctttctggga aagtcaagcc catctatttc cacaccagtg gactcgag 3768

```

<210> 2

<211> 2970

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence construct EA1/TAD

<400> 2

```

accgggactg aaaatgagac atattatctg ccacggaggt gttattaccg aagaaatggc 60
cgccagtctt ttggaccagc tgatcgaaga ggtactggct gataatcttc cacctcctag 120
ccattttgaa ccacctaccc ttcacgaact gtatgattta gacgtgacgg cccccgaaga 180
tcccacagag gaggcggttt cgcagatttt tcccgactct gtaatgttgg cgggtgcagga 240

```

```

agggattgac ttactcactt ttccgcccgc gcccggttct ccggagccgc ctcacctttc 300
ccggcagccc gagcagccgg agcagagagc cttgggtccg gtttctatgc caaaccttgt 360
accggaggtg atcgatctta cctgccacga ggctggcttt ccacccagtg acgacgagga 420
tgaagagggg gaggagtttg tgtagatta tgtggagcac ccggggcacg gttgcaggtc 480
ttgtcattat caccggagga atacggggga cccagatatt atgtgttcgc tttgctatat 540
gaggacctgt ggcattgttg tctacagtaa gtgaaaatta tgggcagtgg gtgatagagt 600
ggtgggtttg gtgtggtaat ttttttttta atttttacag ttttgtggtt taaagaattt 660
tgtattgtga tttttttaaa aggtcctgtg tctgaacctg agcctgagcc cgagccagaa 720
ccggagccctg caagacctac ccgccgtcct aaaatggcgc ctgctatcct gagacgcccg 780
acatcacctg tgtctagaga atgcaatagt agtacggata gctgtgactc cggctccttct 840
aacacacctc ctgagataca cccggtggtc ccgctgtgcc ccattaaacc agttgccgtg 900
agagttgggtg ggcgtcgcca ggctgtggaa tgtatcgagg acttgcttaa cgagcctggg 960
caaccttttg acttgagctg taaacgcccc aggccagcgg ccgcagaagt gcagttaggg 1020
ctgggaaggg tctaccctcg gccgcccgtc aagacctacc gaggagcttt ccagaatctg 1080
ttccagagcg tgcgcgaagt gatccagaac ccgggccccca ggcacccaga ggccgcgagc 1140
gcagcacctc ccggcgccag ttgtctgtcg ctgcagcagc agcagcagca gcagcagca 1200
cagcagcagc agcagcagca gcagcagcag ctagccccag gcagcagcag 1260
cagcagcagg gtgaggatgg ttctcccaa gcccatcgta gaggccccac aggctacctg 1320
gtcctggatg aggaacagca accttcacag ccgcagtcgg ccctggagtg ccaccccgag 1380
agaggttgcg tcccagagcc tggagccgcc gtggccgcca gcaaggggct gccgcagcag 1440
ctgccagcac ctccggacga ggatgactca gctgccccat ccacgttgtc cctgctgggc 1500
cccactttcc ccggcttaag cagctgctcc gctgacctta aagacatcct gagcgaggcc 1560
agcaccatgc aactccttca gcaacagcag caggaagcag tatccgaagg cagcagcagc 1620
gggagagcga gggaggcctc gggggctccc acttctcca aggacaatta cttagggggc 1680
acttcgacca tttctgacaa cgccaaggag ttgtgtaagg cagtgtcggg gtccatgggc 1740
ctgggtgtgg aggcgttgga gcatctgagt ccagggaac agcttcgggg ggattgcatg 1800
tacgcccac ttttgggagt tccaccgct gtgcgtccca ctcttgtgc ccattggcc 1860
gaatgcaaag gttctctgct agacgacagc gcaggcaaga gcaactgaaga tactgctgag 1920
tattccctt tcaagggagg ttacaccaa gggctagaag gcgagagcct aggtctctct 1980
ggcagcgtg cagcagggag ctccgggaca cttgaactgc cgtctaccct gtctctctac 2040
aagtccggag cactggacga ggcagctgcg taccagagtc gcgactacta caactttcca 2100
ctggtctctg ccggaccgcc gcccctccg ccgcctcccc atccccacgc tcgcatcaag 2160
ctggagaacc cgctggacta cggcagcgcc tgggcgggtg cggcggcgca gtgccgtat 2220
ggggacctg cgagcctgca tggcgcggtg gcagcgggac ccggttctgg gtcaccctca 2280
gccgcgctt cctcatcctg gcacactctc ttacagccg aagaaggcca gttgtatgga 2340
ccgtgtggtg gtggtggggg tgggtggcgc ggcggcgccg gcggcgccgg cggcgccggc 2400
ggcgccggcg gcggcgccga ggcgggagct gtagccccct acggctacac tcggccccct 2460
caggggctgg cgggccagga aagcgacttc accgcacctg atgtgtggtg ccctggcgcc 2520
atggtgagca gagtgccta tcccagtcct acttgtgtca aaagcgaaat gggcccctgg 2580
atggatagct actccggacc ttacggggac atgcgtttgg agactgccag ggacctggt 2640
ttgcccattg actattactt tccacccag aagacctgcc tgatctgtgg agatgaagct 2700
tctgggtgtc actatggagc tctcacatgt ggaagctgca aggtcttctt caaaagagcc 2760
gctgaagggg aacagaagta cctgtgcgcc agcagaaatg attgcactat tgataaattc 2820
cgaaggaaaa attgtccatc ttgtcgtctt cggaatgtt atgaagcagg gatgactctg 2880
ggagcccga agctgaagaa acttggtaat ctgaaactac aggaggaagg agaggcttcc 2940
agcaccacca gcccactga gtgactcgag 2970

```

<210> 3

<211> 1305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence construct EA1/DBD

<400> 3

```

accgggactg aaaatgagac atattatctg ccacggaggt gttattaccg aagaaatggc 60
cgccagtctt ttggaccagc tgatcgaaga ggtactggct gataatcttc cacctcctag 120
ccattttgaa ccacctaccc ttcacgaact gtatgattta gacgtgacgg cccccgaaga 180
tcccacagag gaggcgggtt cgcagatttt tcccgaactct gtaatgttgg cgggtgcagga 240
agggattgac ttactcactt ttccgccggc gcccggttct ccggagccgc ctcacctttc 300
ccggcagccc gagcagccgg agcagagagc cttgggtccg gtttctatgc caaaccttgt 360
accggaggtg atcgatctta cctgccacga ggctggcttt ccacccagtg acgacgagga 420
tgaagagggg gaggagtttg tgtagatta tgtggagcac cccgggcacg gttgcaggtc 480
ttgtcattat caccggagga atacggggga cccagatatt atgtgttcgc tttgctatat 540
gaggacctgt ggcattgttg tctacagtaa gtgaaaatta tgggcagtgg gtgatagagt 600
ggtgggtttg gtgtggtaat ttttttttta atttttacag ttttgtggtt taaagaattt 660
tgtattgtga tttttttaaa aggtcctgtg tctgaacctg agcctgagcc cgagccagaa 720
ccggagcctg caagacctac ccgcgcctct aaaatggcgc ctgctatcct gagacgcccg 780
acatcacctg tgtctagaga atgcaatagt agtacggata gctgtgactc cggtccttct 840
aacacacctc ctgagataca cccggtggtc ccgctgtgcc ccattaaacc agttgccgtg 900
agagttgggt ggcgtcgcca ggctgtggaa tgtatcgagg acttgcttaa cgagcctggg 960
caaccttttg acttgagctg taaacgcccc aggccagcgg ccgcaaagac ctgcctgac 1020
tgtggagatg aagcttctgg gtgtcactat ggagctctca catgtggaag ctgcaaggtc 1080
ttcttcaaaa gagccgctga agggaaacag aagtacctgt gcgccagcag aaatgattgc 1140
actattgata aattccgaag gaaaaattgt ccattctgtc gtcttcggaa atgttatgaa 1200
gcagggatga ctctgggagc ccggaagctg aagaaacttg gtaatctgaa actacaggag 1260
gaaggagagg cttccagcac caccagcccc actgagtgac tcgag 1305

```

<210> 4

<211> 3514

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence construct 12S/AR

<400> 4

```

accgggactg aaaatgagac atattatctg ccacggaggt gttattaccg aagaaatggc 60
cgccagtctt ttggaccagc tgatcgaaga ggtactggct gataatcttc cacctcctag 120
ccattttgaa ccacctaccc ttcacgaact gtatgattta gacgtgacgg cccccgaaga 180
tcccacagag gaggcgggtt cgcagatttt tcccgaactct gtaatgttgg cgggtgcagga 240
agggattgac ttactcactt ttccgccggc gcccggttct ccggagccgc ctcacctttc 300
ccggcagccc gagcagccgg agcagagagc cttgggtccg gtttctatgc caaaccttgt 360
accggaggtg atcgatctta cctgccacga ggctggcttt ccacccagtg acgacgagga 420
tgaagagggg cctgtgtctg aacctgagcc tgagcccgag ccagaaccgg agcctgcaag 480
acctaccgcg cgtcctaaaa tggcgctgc tatcctgaga cgcccacat cacctgtgtc 540
tagagaatgc aatagtagta cggatagctg tgactccggg ccttctaaca cacctcctga 600
gatacacccg gtgggtccgc tgtgccccat taaaccagtt gccgtgagag ttgggtgggcg 660
tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac ctttggactt 720
gagctgtaaa cgccccaggc cagcggccgc agaagtgcag ttagggctgg gaagggtcta 780
ccctcgcccg ccgtccaaga cctaccgagg agctttccag aatctgttcc agagcgtgcg 840
cgaagtgatc cagaaccggg gccccaggca cccagaggcc gcgagcgag cacctcccgg 900

```

cgccagtttg	ctgctgctgc	agcagcagca	gcagcagcag	cagcagcagc	agcagcagca	960
gcagcagcag	cagcagcagc	aagagactag	ccccaggcag	cagcagcagc	agcaggggtga	1020
ggatggttct	ccccaaagccc	atcgtagagg	ccccacaggc	tacctgggtcc	tggatgagga	1080
acagcaacct	tcacagccgc	agtcggccct	ggagtgccac	cccagagagag	gttgcggtccc	1140
agagcctgga	gccgccgtgg	ccgccagcaa	ggggctgccg	cagcagctgc	cagcacctcc	1200
ggacgaggat	gactcagctg	ccccatccac	gttggtccctg	ctggggcccca	ctttccccgg	1260
cttaagcagc	tgctccgctg	accttaaaga	catcctgagc	gaggccagca	ccatgcaact	1320
ccttcagcaa	cagcagcagg	aagcagtatc	cgaaggcagc	agcagcggga	gagcgagggga	1380
ggcctcgggg	gctcccactt	cctccaagga	caattactta	gggggcactt	cgaccatttc	1440
tgacaacgcc	aaggagtgtg	gtaaggcagt	gtcgggtgtcc	atgggcctgg	gtgtggaggc	1500
gttggagcat	ctgagtccag	gggaacagct	tcggggggat	tgcagtacg	ccccactttt	1560
gggagttcca	cccgtgtg	gtcccactcc	ttgtgcccc	ttggccgaat	gcaaagggttc	1620
tctgctagac	gacagcgag	gcaagagcac	tgaagatact	gctgagtatt	cccctttcaa	1680
gggaggttac	accaaagggc	tagaaggcga	gagcctaggc	tgctctggca	gcgctgcagc	1740
agggagctcc	gggacacttg	aactgccgtc	taacctgtct	ctctacaagt	ccggagcact	1800
ggacgaggca	gctgcgtacc	agagtgcgca	ctactacaac	tttccactgg	ctctggccgg	1860
accgccgccc	cctccgcgcg	ctccccatcc	ccacgctcgc	atcaagctgg	agaaccgcgt	1920
ggactacggc	agcgccctggg	cggctgcggc	ggcgagctgc	cgctatgggg	acctggcgag	1980
cctgcatggc	gcgggtgcag	cgggaccggg	ttctgggtca	ccctcagccg	ccgcttcctc	2040
atcctggcac	actctcttca	cagccgaaga	aggccagttg	tatggaccgt	gtggtgggtgg	2100
tgggggtggt	ggcgggcg	gcggcgggcg	cggcgggcg	ggcgggcg	gcggcgggcg	2160
cggcgaggcg	ggagctgtag	ccccctacgg	ctacactcgg	ccccctcagg	ggctggcggg	2220
ccaggaaagc	gacttcaccg	cacctgatgt	gtggtaccct	ggcggcattg	tgagcagagt	2280
gccctatccc	agtcccactt	gtgtcaaaa	cgaaatgggc	ccctggatgg	atagctactc	2340
cggaccttac	ggggacatgc	gtttggagac	tgccagggac	catgttttgc	ccattgacta	2400
ttactttcca	cccagaaga	cctgcctgat	ctgtggagat	gaagcttctg	aaggtcacta	2460
tggagctctc	acatgtggaa	gctgcaagg	cttcttcaaa	agagccgctg	aggggaaaca	2520
gaagtacctg	tgcgccagca	gaaatgattg	cactattgat	aaattccgaa	ggaaaaattg	2580
tccatcttgt	cgtcttcgga	aatgttatga	agcagggatg	actctgggag	cccgggaagt	2640
gaagaaactt	ggtaatctga	aactacagga	ggaaggagag	gcttcagca	ccaccagccc	2700
cactgaggag	acaaccaga	agctgacagt	gtcacacatt	gaaggctatg	aatgtcagcc	2760
catctttctg	aatgtcctgg	aagccattga	gccagggtga	gtgtgtgctg	gacacgacaa	2820
caaccagccc	gactcctttg	cagccttgct	ctctagcctc	aatgaactgg	gagagagaca	2880
gcttgtagac	gtgggtcaagt	gggccaaggc	cttgccctggc	ttccgcaact	tacacgtgga	2940
cgaccagatg	gctgtcattc	agtactcctg	gatggggctc	atgggtgttg	ccatgggctg	3000
gcgatacctc	accaatgtca	actccaggat	gctctacttc	gcccctgata	tggttttcaa	3060
tgagtaccgc	atgcacaagt	cccgatgta	cagccagtgt	gtccgaatga	ggcacctctc	3120
tcaagagttt	ggatggctcc	aaatcacccc	ccagggaattc	ctgtgcatga	aagcactgct	3180
actcttcagc	attattccag	tggatgggct	gaaaaatcaa	aaattctttg	atgaacttcg	3240
aatgaactac	atcaaggaac	tcgatcgtat	cattgcatgc	aaaagaaaaa	atcccacatc	3300
ctgctcaaga	cgcttctacc	agctcaccaa	gctcctggac	tccgtgcagc	ctattgcgag	3360
agagctgcat	cagttcactt	ttgacctgct	aatcaagtca	cacatgggtga	gcgtggactt	3420
tccggaaatg	atggcagaga	tcattctctg	gcaagtgcgc	aagatccttt	ctgggaaagt	3480
caagcccatc	tatttccaca	cccagtgact	cgag			3514

<210> 5

<211> 2716

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence construct 12S/TAD

<400> 5

```

accgggactg aaaatgagac atattatctg ccacggaggt gttattaccg aagaaatggc 60
cgccagtctt ttggaccagc tgatcgaaga ggtactggct gataatcttc cacctcctag 120
ccattttgaa ccacctaccc ttcacgaact gtatgattta gacgtgacgg cccccgaaga 180
tcccaacgag gaggcgggtt cgcagatttt tcccgaactt gtaatgttgg cgggtgcagga 240
agggattgac ttactcaact ttccgcccgc gcccggttct ccggagccgc ctcacctttc 300
ccggcagccc gagcagccgg agcagagagc cttgggtccg gtttctatgc caaaccttgt 360
accggaggtg atcgatctta cctgccacga ggtgggtctt ccacccagtg acgacgagga 420
tgaagaggtt cctgtgtctg aacctgagcc tgagcccag ccagaaccgg agcctgcaag 480
acctacccgc cgtcctaaaa tggcgccctg tatectgaga cgcccacat cacctgtgtc 540
tagagaatgc aatagtagta cggatagctg tgactccggc ctttctaaca cacctcctga 600
gatacacccg gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggag 660
tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac ctttggactt 720
gagctgtaaa cgccccaggc cagcggccgc agaagtgcag ttagggctgg gaagggctta 780
ccctcgcccg ccgtccaaga cctaccgagg agctttccag aatctgttcc agagcgtgag 840
cgaagtgatc cagaaccggg gccccaggca ccagagggc gcgagcgag cacctcccgg 900
cgccagttag ctgctgtctg agcagcagc cagcagcagc agcagcagc agcagcagc 960
gcagcagcag cagcagcagc aagagactag ccccaggcag cagcagcagc agcagggtag 1020
ggatgggttct ccccaagccc atcgtagagg cccacaggc tacctgggtc tggatgagga 1080
acagcaacct tcacagccgc agtcggccct ggagtgccac cccgagagag gttgcgtccc 1140
agagcctgga gccgcccgtg ccgccagcaa ggggctgccg cagcagctgc cagcacctcc 1200
ggacgaggat gactcagctg ccccatccac gttgtccctg ctgggccccca ctttccccgg 1260
cttaagcagc tgctccgctg accttaaaga catcctgagc gaggccagca ccatgcaact 1320
ccttcagcaa cagcagcagg aagcagtatc cgaaggcagc agcagcggga gagcagggga 1380
ggcctcgggg gctcccactt cctccaagga caattactta gggggcactt cgaccatttc 1440
tgacaacgcc aaggagtgtg gtaaggcagt gtcgggtgtc atgggcctgg gtgtggaggc 1500
gttggagcat ctgagtccag gggaacagct tcggggggat tgcagttagc cccactttt 1560
gggagtcca cccgctgtgc gteccactcc ttgtgccccca ttggccgaat gcaaagggtc 1620
tctgctagac gacagcgcag gcaagagcac tgaagatact gctgagtatt cccctttcaa 1680
gggaggttac accaaagggc tagaaggcga gagcctaggc tgctctggca gcgctgcagc 1740
agggagctcc gggacacttg aactgccgtc taccctgtct ctctacaagt ccggagcact 1800
ggacgaggga gctgcgtacc agagtcgcga ctactacaac tttccactgg ctctggccgg 1860
accgccgccc cctccgcccgc ctccccatcc ccacgctcgc atcaagctgg agaaccgct 1920
ggactacggc agcgcctggg cggctgcggc ggcgcagtgc cgctatgggg acctggcgag 1980
cctgcatggc gcgggtgcag cgggacccgg ttctgggtca ccctcagccg ccgcttcctc 2040
atcctggcac actctcttca cagccgaaga aggccagttg tatggaccgt gtggtggtgg 2100
tggggggtgt ggccggcgcg gcggcgccgc cggcgccggc ggccggcgcg gcggcgccgc 2160
cggcgaggcg ggagctgtag cccctacgg ctacactcgg cccctcagg ggctggcggg 2220
ccaggaaagc gacttcaccg cacctgatgt gtggtaccct ggccgcatgg tgagcagagt 2280
gccctatccc agtcccactt gtgtcaaaaag cgaaatgggc ccctggatgg atagctactc 2340
cggaccttac ggggacatgc gtttggagac tgccagggac catgttttgc ccattgacta 2400
ttactttcca cccagaaga cctgcctgat ctgtggagat gaagcttctg ggtgtcacta 2460
tgagctctc acatgtgga gctgcaaggc cttcttcaaa agagccgctg aagggaaaca 2520
gaagtacctg tgcgccagca gaaatgattg cactattgat aaattccgaa ggaaaaattg 2580
tccatcttgt cgtcttcgga aatgttatga agcagggatg actctgggag cccggaagct 2640
gaagaaactt ggtaatctga aactacagga ggaaggagag gcttccagca ccaccagccc 2700
cactgagtga ctcgag

```

<210> 6

<211> 1051

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence construct 12S/DBD

<400> 6

```

accgggactg aaaatgagac atattatctg ccacggagggt gttattaccg aagaaatggc 60
cgccagtctt ttggaccagc tgatcgaaga ggtactggct gataatcttc cacctcctag 120
ccatthttgaa ccacctaccc ttcacgaact gtatgattta gacgtgacgg cccccgaaga 180
tcccaacgag gaggcgggtt cgcagatttt tcccgactct gtaatgttgg cgggtgcagga 240
agggattgac ttactcactt ttccgccggc gcccggttct ccggagccgc ctcacctttc 300
ccggcagccc gagcagccgg agcagagagc cttgggtccg gtttctatgc caaaccttgt 360
accggagggt atcgatctta cctgccacga ggctggcttt ccaccagtg acgacgagga 420
tgaagagggt cctgtgtctg aacctgagcc tgagcccagc ccagaaccgg agcctgcaag 480
acctacccgc cgtcctaaaa tggcgccctg tctcctgaga cgcccacat cacctgtgtc 540
tagagaatgc aatagtagta cggatagctg tgactccggt ccttctaaca cacctcctga 600
gatacacccg gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggag 660
tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac ctttgactt 720
gagctgtataa cgcccaggc cagcgccgc aaagacctgc ctgatctgtg gagatgaagc 780
ttctgggtgt cactatggag ctctcacatg tggaaactgc aaggtcttct tcaaaagagc 840
cgctgaaggg aaacagaagt acctgtgcgc cagcagaaat gattgacta ttgataaatt 900
ccgaaggaaa aattgtccat cttgtcgtct tcggaaatgt tatgaagcag ggatgactct 960
gggagcccgg aagctgaaga aacttggtta tctgaaacta caggaggaag gagaggcttc 1020
cagcaccacc agccccactg agtgactcga g                                     1051

```

<210> 7

<211> 1164

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
amino acid sequence construct 12S/AR

<400> 7

```

Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
  1             5             10             15

```

```

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
      20             25             30

```

```

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu Tyr Asp
  35             40             45

```

```

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
  50             55             60

```

```

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
  65             70             75             80

```

```

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
      85             90             95

```

8/20

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly
115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Pro Val Ser Glu Pro
130 135 140

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg
145 150 155 160

Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser
165 170 175

Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn
180 185 190

Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro
195 200 205

Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu
210 215 220

Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg
225 230 235 240

Pro Arg Pro Ala Ala Ala Glu Val Gln Leu Gly Leu Gly Arg Val Tyr
245 250 255

Pro Arg Pro Pro Ser Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe
260 265 270

Gln Ser Val Arg Glu Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu
275 280 285

Ala Ala Ser Ala Ala Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln
290 295 300

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
305 310 315 320

Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu
325 330 335

Asp Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val
340 345 350

Leu Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys
355 360 365

His Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala
370 375 380

9/20

Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp
385 390 395 400

Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly
405 410 415

Leu Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser
420 425 430

Thr Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly
435 440 445

Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser
450 455 460

Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys
465 470 475 480

Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala
485 490 495

Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr
500 505 510

Ala Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala
515 520 525

Pro Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys
530 535 540

Ser Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr
545 550 555 560

Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala
565 570 575

Gly Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys
580 585 590

Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr
595 600 605

Asn Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro
610 615 620

His Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser
625 630 635 640

Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser
645 650 655

Leu His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala
660 665 670

10/20

Ala	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln		
		675					680					685					
Leu	Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
	690					695						700					
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	
705					710					715						720	
Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly		
				725					730						735		
Gln	Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met		
			740					745					750				
Val	Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met		
		755					760					765					
Gly	Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu		
	770					775					780						
Glu	Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro		
785					790					795					800		
Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr		
				805					810					815			
Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala		
			820					825					830				
Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile		
		835					840					845					
Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys		
	850					855					860						
Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly		
865					870					875					880		
Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro		
				885					890					895			
Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr		
				900				905					910				
Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly		
		915					920					925					
Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala		
	930					935					940						
Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val		
945					950					955					960		

11/20

Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp
965 970 975

Asp Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe
980 985 990

Ala Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr
995 1000 1005

Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg
1010 1015 1020

Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly
1025 1030 1035 1040

Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu
1045 1050 1055

Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe
1060 1065 1070

Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala
1075 1080 1085

Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu
1090 1095 1100

Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln
1105 1110 1115 1120

Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe
1125 1130 1135

Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu
1140 1145 1150

Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln
1155 1160

<210> 8

<211> 898

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
amino acid sequence construct 12S/TAD

<400> 8

Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1 5 10 15

12/20

Ala	Ser	Leu	Leu	Asp	Gln	Leu	Ile	Glu	Glu	Val	Leu	Ala	Asp	Asn	Leu		
			20					25					30				
Pro	Pro	Pro	Ser	His	Phe	Glu	Pro	Pro	Thr	Leu	His	Glu	Leu	Tyr	Asp		
		35					40					45					
Leu	Asp	Val	Thr	Ala	Pro	Glu	Asp	Pro	Asn	Glu	Glu	Ala	Val	Ser	Gln		
	50					55					60						
Ile	Phe	Pro	Asp	Ser	Val	Met	Leu	Ala	Val	Gln	Glu	Gln	Ile	Asp	Leu		
65					70					75					80		
Leu	Thr	Phe	Pro	Pro	Ala	Pro	Gly	Ser	Pro	Glu	Pro	Pro	His	Leu	Ser		
				85					90					95			
Arg	Gln	Pro	Glu	Gln	Pro	Glu	Gln	Arg	Ala	Leu	Gly	Pro	Val	Ser	Met		
			100					105					110				
Pro	Asn	Leu	Val	Pro	Glu	Val	Ile	Asp	Leu	Thr	Cys	His	Glu	Ala	Gly		
		115					120					125					
Phe	Pro	Pro	Ser	Asp	Asp	Glu	Asp	Glu	Glu	Gly	Pro	Val	Ser	Glu	Pro		
	130					135					140						
Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Ala	Arg	Pro	Thr	Arg	Arg		
145					150					155					160		
Pro	Lys	Met	Ala	Pro	Ala	Ile	Leu	Arg	Arg	Pro	Thr	Ser	Pro	Val	Ser		
				165					170					175			
Arg	Glu	Cys	Asn	Ser	Ser	Thr	Asp	Ser	Cys	Asp	Ser	Gly	Pro	Ser	Asn		
			180					185					190				
Thr	Pro	Pro	Glu	Ile	His	Pro	Val	Val	Pro	Leu	Cys	Pro	Ile	Lys	Pro		
		195					200					205					
Val	Ala	Val	Arg	Val	Gly	Gly	Arg	Arg	Gln	Ala	Val	Glu	Cys	Ile	Glu		
	210					215					220						
Asp	Leu	Leu	Asn	Glu	Pro	Gly	Gln	Pro	Leu	Asp	Leu	Ser	Cys	Lys	Arg		
225					230					235					240		
Pro	Arg	Pro	Ala	Ala	Ala	Glu	Val	Gln	Leu	Gly	Leu	Gly	Arg	Val	Tyr		
				245					250					255			
Pro	Arg	Pro	Pro	Ser	Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe		
			260					265					270				
Gln	Ser	Val	Arg	Glu	Val	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu		
		275					280					285					
Ala	Ala	Ser	Ala	Ala	Pro	Pro	Gly	Ala	Ser	Leu	Leu	Leu	Leu	Gln	Gln		
	290					295					300						

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 305 310 315 320

Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu
 325 330 335

Asp Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val
 340 345 350

Leu Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys
 355 360 365

His Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala
 370 375 380

Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp
 385 390 395 400

Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly
 405 410 415

Leu Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser
 420 425 430

Thr Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly
 435 440 445

Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser
 450 455 460

Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys
 465 470 475 480

Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala
 485 490 495

Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr
 500 505 510

Ala Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala
 515 520 525

Pro Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys
 530 535 540

Ser Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr
 545 550 555 560

Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala
 565 570 575

Gly Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys
 580 585 590

14/20

Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	595	600	605	
Asn	Phe	Pro	Leu	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	610	615	620	
His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	625	630	635	640
Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	645	650	655	
Leu	His	Gly	Ala	Gly	Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	660	665	670	
Ala	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	675	680	685	
Leu	Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	690	695	700	
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	705	710	715	720
Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	725	730	735	
Gln	Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	740	745	750	
Val	Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	755	760	765	
Gly	Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	770	775	780	
Glu	Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	785	790	795	800
Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	805	810	815	
Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	820	825	830	
Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	835	840	845	
Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	850	855	860	
Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	865	870	875	880

15/20

Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro
885 890 895

Thr Glu

<210> 9

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
amino acid sequence construct 12S/DBD

<400> 9

Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu Tyr Asp
35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly
115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Pro Val Ser Glu Pro
130 135 140

Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg
145 150 155 160

Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser
165 170 175

Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn
180 185 190

16/20

Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro
195 200 205

Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu
210 215 220

Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg
225 230 235 240

Pro Arg Pro Ala Ala Ala Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala
245 250 255

Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe
260 265 270

Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg
275 280 285

Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys
290 295 300

Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys
305 310 315 320

Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser
325 330 335

Ser Thr Thr Ser Pro Thr Glu
340

<210> 10
<211> 986
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence construct EA1

<400> 10
atgagacata ttatctgcca cggaggtggt attaccgaag aaatggccgc cagtcttttg 60
gaccagctga tcgaagaggt actggctgat aatcttccac ctccctagcca ttttgaacca 120
cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agatttttcc cgactctgta atgttggcgg tgcaggaagg gattgactta 240
ctcacttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccag 300
cagccggagc agagagcctt gggtcgggtt tctatgccaa accttgtacc ggaggtgatc 360
gatcttacct gccacgaggc tggctttcca cccagtgaag acgaggatga agaggggtgag 420
gagtttgtgt tagattatgt ggagcacccc gggcacgggt gcaggtcttg tcattatcac 480
cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggg gggtttggtg 600
tggttaattt ttttttaatt ttacagttt tgtggtttta agaattttgt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
gacctaccgc ccgtcctaaa atggcgctg ctatcctgag acgcccgcga tcacctgtgt 780


```

ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccg ggtgggtccc ctgtgcccc ttaaaccagt tgccgtgaga gttgggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
tgagctgtaa acgccccagg ccataa 986

```

<210> 11
 <211> 986
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide sequence construct EA1/TAD

```

<400> 11
atgagacata ttatctgcca cggaggtggt attaccgaag aaatggccgc cagtcttttg 60
gaccagctga tcgaagaggt actggctgat aatcttccac ctccatagcca ttttgaacca 120
cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agatttttcc cgactctgta atgttgccg tgcaggaagg gattgactta 240
ctcacttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccag 300
cagccggagc agagagcctt gggtcgggtt tctatgccaa accttgtacc ggaggtgatc 360
gatcttacct gccacgaggc tggctttcca cccagtgcag acgaggatga agaggggtgag 420
gagtttgtgt tagattatgt ggagcaccgc gggcacgggt gcaggtcttg tcattatcac 480
cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggg gggtttggtg 600
tggttaattt ttttttaatt tttacagttt tgtggtttta agaattttgt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
gacctaccgc ccgtcctaaa atggcgcttg ctatcctgag acgcccgcgc tcacctgtgt 780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccg ggtgggtccc ctgtgcccc ttaaaccagt tgccgtgaga gttgggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960
tgagctgtaa acgccccagg ccataa 986

```

<210> 12
 <211> 1022
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide sequence construct EA1/AR

```

<400> 12
atgagacata ttatctgcca cggaggtggt attaccgaag aaatggccgc cagtcttttg 60
gaccagctga tcgaagaggt actggctgat aatcttccac ctccatagcca ttttgaacca 120
cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agatttttcc cgactctgta atgttgccg tgcaggaagg gattgactta 240
ctcacttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccag 300
cagccggagc agagagcctt gggtcgggtt tctatgccaa accttgtacc ggaggtgatc 360
gatcttacct gccacgaggc tggctttcca cccagtgcag acgaggatga agaggggtgag 420
gagtttgtgt tagattatgt ggagcaccgc gggcacgggt gcaggtcttg tcattatcac 480
cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540

```

```

atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggg gggtttggtg 600
tggtaatatt ttttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
gacctaccgg ccgtcctaaa atggcgccgt ctatcctgag acgcccgcaca tcacctgtgt 780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccg ggtggtcccg ctgtgcccc aataaccagt tgccgtgaga gttggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa ctttggact 960
tgagctgtaa acgccccagg ccataagcgg ccgcagaagt gcagttaggg ctgggaaggg 1020
tc

```

<210> 13

<211> 1022

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence construct EA1/AR(C685Y)

<400> 13

```

atgagacata ttatctgcca cggaggtggt attaccgaag aaatggccgc cagtcttttg 60
gaccagctga tcgaagaggt actggtgat aatcttccac ctctagcca tttgaacca 120
cctacccttc acgaactgta tgatttagac gtgacggccc ccgaagatcc caacgaggag 180
gcggtttcgc agatttttcc cgactctgta atgttggcgg tgcaggaagg gattgactta 240
ctcacttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccgag 300
cagccggagc agagagcctt gggtcgggtt tctatgcaa accttgtagc ggaggtgatc 360
gatcttacct gccacgagc tggctttcca cccagtgcg acgaggatga agagggtgag 420
gagtttgtgt tagattatgt ggagcaccgc gggcacggtt gcaggtcttg tcattatcac 480
cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc 540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggg gggtttggtg 600
tggtaatatt ttttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt 660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720
gacctaccgg ccgtcctaaa atggcgccgt ctatcctgag acgcccgcaca tcacctgtgt 780
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaac acacctcctg 840
agatacaccg ggtggtcccg ctgtgcccc aataaccagt tgccgtgaga gttggtgggc 900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa ctttggact 960
tgagctgtaa acgccccagg ccataagcgg ccgcagaagt gcagttaggg ctgggaaggg 1020
tc

```

<210> 14

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 14

tcactcggat ccaccgggac tgaaaatgag acatat

36

<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 15
tacatcactc gcggccgctg gcctggggcg ttacagctc a 41

<210> 16
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 16
tacatcactc gcggccgcag aagtcagtt agggctggga a 41

<210> 17
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 17
tcactcctcg agtcactggg tgtggaaata gatgggctt 39

<210> 18
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 18
tacatcactc gcggccgcag aagtcagtt agggctggga a 41

<210> 19
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 19
tcactcctcg agtcactcag tggggctggt ggtgctgga

39

<210> 20
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 20
tacatcactc gcggccgcaa agacctgcct gatctgtgga gat

43

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 21
cccaagcttt ccttctaaca cacctcctg

29

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 22
cgggatccga ggtcagatgt aaccaaga

28

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☒ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER: _____**

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.